

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/712,629C
Source: 1Fg/16
Date Processed by STIC: 5/2/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/7/2, 629C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | | | |
|----|------|------------------------------------|---|
| 1 | ____ | Wrapped Nucleics
Wrapped Aminos | The number/text at the end of each line “wrapped” down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent “wrapping.” |
| 2 | ____ | Invalid Line Length | The rules require that a line not exceed 72 characters in length. This includes white spaces. |
| 3 | ____ | Misaligned Amino
Numbering | The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead. |
| 4 | ____ | Non-ASCII | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. |
| 5 | ____ | Variable Length | Sequence(s) ____ contain n’s or Xaa’s representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. |
| 6 | ____ | PatentIn 2.0
“bug” | A “bug” in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. |
| 7 | ____ | Skipped Sequences
(OLD RULES) | Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where “X” is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where “X” is shown)
This sequence is intentionally skipped
Please also adjust the “(ii) NUMBER OF SEQUENCES:” response to include the skipped sequences. |
| 8 | ____ | Skipped Sequences
(NEW RULES) | Sequence(s) ____ missing. If intentional , please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 |
| 9 | ____ | Use of n’s or Xaa’s
(NEW RULES) | Use of n’s and/or Xaa’s have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n’s or Xaa’s are present.
In <220> to <223> section, please explain location of n or Xaa , and which residue n or Xaa represents. |
| 10 | ____ | Invalid <213>
Response | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below) |
| 11 | ____ | Use of <220> | Sequence(s) ____ missing the <220> “Feature” and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> “Organism” response is “Artificial Sequence” or “Unknown.” Please explain source of genetic material in <220> to <223> section or use “chemically synthesized” as explanation. (See “Federal Register,” 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules |
| 12 | ____ | PatentIn 2.0
“bug” | Please do not use “Copy to Disk” function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use “File Manager” or any other manual means to copy file to floppy disk. |
| 13 | ____ | Misuse of n/Xaa | “n” can only represent a single nucleotide; “Xaa” can only represent a single <u>amino acid</u> |



IFW16

RAW SEQUENCE LISTING

DATE: 05/02/2006

PATENT APPLICATION: US/10/712,629C

TIME: 14:30:25

Input Set : A:\PTO.TS.txt

Output Set: N:\CRF4\05022006\J712629C.raw

3 <110> APPLICANT: The Procter & Gamble Company
 5 <120> TITLE OF INVENTION: Composition Comprising a Mouse HRT Protein Human
 6 Interacting Partner Protein Complex
 8 <130> FILE REFERENCE: 9423
 10 <140> CURRENT APPLICATION NUMBER: US 10/712,629C
 11 <141> CURRENT FILING DATE: 2003-11-13
 13 <160> NUMBER OF SEQ ID NOS: 20
 15 <170> SOFTWARE: PatentIn version 3.3

pp 1,3-5
**Does Not Comply
 Corrected Diskette Needed**

ERRORED SEQUENCES

523 <210> SEQ ID NO: 17
 524 <211> LENGTH: 2079
 525 <212> TYPE: DNA
 526 <213> ORGANISM: Nucleotide sequence of HRT corresponding to the amino acid residue

490-
 W--> 527 1182 of the C-terminal portion of HR protein

529 <400> SEQUENCE: 17
 531 Val Thr Gln Cys Gln Ser Cys Val Gln Ala Ala Gly Glu Val Gly Val
 532 1 5 10 15
 535 Leu Thr Gly His Ser Gln Lys Ser Arg Arg Ser Pro Leu Glu Glu Lys
 536 20 25 30
 539 Gln Leu Glu Glu Glu Asp Ser Ser Ala Thr Ser Glu Glu Gly Gly Gly
 540 35 40 45
 543 Gly Pro Gly Pro Glu Ala Ser Leu Asn Lys Gly Leu Ala Lys His Leu
 544 50 55 60
 547 Leu Ser Gly Leu Gly Asp Arg Leu Cys Arg Leu Leu Arg Lys Glu Arg
 548 65 70 75 80
 551 Glu Ala Leu Ala Trp Ala Gln Arg Glu Gly Gln Gly Pro Ala Met Thr
 552 85 90 95
 555 Glu Asp Ser Pro Gly Ile Pro His Cys Cys Ser Arg Cys His His Gly
 556 100 105 110
 559 Leu Phe Asn Thr His Trp Arg Cys Ser His Cys Ser His Arg Leu Cys
 560 115 120 125
 563 Val Ala Cys Gly Arg Ile Ala Gly Ala Gly Lys Asn Arg Glu Lys Thr
 564 130 135 140
 567 Gly Ser Gln Glu Gln His Thr Asp Asp Cys Ala Gln Glu Ala Gly His
 568 145 150 155 160
 571 Ala Ala Cys Ser Leu Ile Leu Thr Gln Phe Val Ser Ser Gln Ala Leu
 572 165 170 175
 575 Ala Glu Leu Ser Thr Val Met His Gln Ala Trp Ala Lys Phe Asp Ile
 576 180 185 190
 579 Arg Gly His Cys Phe Cys Gln Val Asp Ala Arg Val Trp Ala Pro Gly

invalid
<213> response
(see item 10
on Euro
summary
sheet)

RAW SEQUENCE LISTING

DATE: 05/02/2006

PATENT APPLICATION: US/10/712,629C

TIME: 14:30:25

Input Set : A:\PTO.TS.txt

Output Set: N:\CRF4\05022006\J712629C.raw

```

580          195          200          205
583 Asp Gly Gly Gln Gln Lys Glu Pro Thr Glu Lys Thr Pro Pro Thr Pro
584          210          215          220
587 Gln Pro Ser Cys Asn Gly Asp Ser Asn Arg Thr Lys Asp Ile Lys Glu
588 225          230          235          240
591 Glu Thr Pro Asp Ser Thr Glu Ser Pro Ala Glu Asp Gly Ala Gly Arg
592          245          250          255
595 Ser Pro Leu Pro Cys Pro Ser Leu Cys Glu Leu Leu Ala Ser Thr Ala
596          260          265          270
599 Val Lys Leu Cys Leu Gly His Asp Arg Ile His Met Ala Phe Ala Pro
600          275          280          285
603 Val Thr Pro Ala Leu Pro Ser Asp Asp Arg Ile Thr Asn Ile Leu Asp
604          290          295          300
607 Ser Ile Ile Ala Gln Val Val Glu Arg Lys Ile Gln Glu Lys Ala Leu
608 305          310          315          320
611 Gly Pro Gly Leu Arg Ala Gly Ser Gly Leu Arg Lys Gly Leu Ser Leu
612          325          330          335
615 Pro Leu Ser Pro Val Arg Thr Arg Leu Ser Pro Pro Gly Ala Leu Leu
616          340          345          350
619 Trp Leu Gln Glu Pro Arg Pro Lys His Gly Phe His Leu Phe Gln Glu
620          355          360          365
623 His Trp Arg Gln Gly Gln Pro Val Leu Val Ser Gly Ile Gln Lys Thr
624          370          375          380
627 Leu Arg Leu Ser Leu Trp Gly Met Glu Ala Leu Gly Thr Leu Gly Gly
628 385          390          395          400
631 Gln Val Gln Ser Leu Thr Ala Leu Gly Pro Pro Gln Pro Thr Asn Leu
632          405          410          415
635 Asp Ser Thr Ala Phe Trp Glu Gly Phe Ser His Pro Glu Thr Arg Pro
636          420          425          430
639 Lys Leu Asp Glu Gly Ser Val Leu Leu Leu His Arg Thr Leu Gly Asp
640          435          440          445
643 Lys Asp Ala Ser Arg Val Gln Asn Leu Val Ser Ser Leu Pro Leu Pro
644          450          455          460
647 Glu Tyr Cys Ala His Gln Gly Lys Leu Asn Leu Ala Ser Tyr Leu Pro
648 465          470          475          480
651 Leu Gly Leu Thr Leu His Pro Leu Glu Pro Gln Leu Trp Ala Ala Tyr
652          485          490          495
655 Gly Val Asn Ser His Arg Gly His Leu Gly Thr Lys Asn Leu Cys Val
656          500          505          510
659 Glu Val Ser Asp Leu Ile Ser Ile Leu Val His Ala Glu Ala Gln Leu
660          515          520          525
663 Pro Pro Trp Tyr Arg Ala Gln Lys Asp Phe Leu Ser Gly Leu Asp Gly
664          530          535          540
667 Glu Gly Leu Trp Ser Pro Gly Ser Gln Thr Ser Thr Val Trp His Val
668 545          550          555          560
671 Phe Arg Ala Gln Asp Ala Gln Arg Ile Arg Arg Phe Leu Gln Met Val
672          565          570          575
675 Cys Pro Ala Gly Ala Gly Thr Leu Glu Pro Gly Ala Pro Gly Ser Cys
676          580          585          590

```

RAW SEQUENCE LISTING

DATE: 05/02/2006

PATENT APPLICATION: US/10/712,629C

TIME: 14:30:25

Input Set : A:\PTO.TS.txt

Output Set: N:\CRF4\05022006\J712629C.raw

679 Tyr Leu Asp Ala Gly Leu Arg Arg Arg Leu Arg Glu Glu Trp Gly Val
 680 595 600 605
 683 Ser Cys Trp Thr Leu Leu Gln Ala Pro Gly Glu Ala Val Leu Val Pro
 684 610 615 620
 687 Ala Gly Ala Pro His Gln Val Gln Gly Leu Val Ser Thr Ile Ser Val
 688 625 630 635 640
 691 Thr Gln His Phe Leu Ser Pro Glu Thr Ser Ala Leu Ser Ala Gln Leu
 692 645 650 655
 695 Cys His Gln Gly Ala Ser Leu Pro Pro Asp His Arg Met Leu Tyr Ala
 696 660 665 670
 699 Gln Met Asp Arg Ala Val Phe Gln Ala Val Lys Ala Ala Val Gly Ala
 700 675 680 685

703 Leu Gln Glu Ala Lys

E--> 704 690

707 <210> SEQ ID NO: 18

708 <211> LENGTH: 693

709 <212> TYPE: PRT ? This is a DNA sequence

710 <213> ORGANISM: C-terminal portion of hairless protein of mouse (HRT) having amino

acid

W--> 711 residues 490 to 1182

713 <400> SEQUENCE: 18

715	gttaccacagt	gccaaagctg	tgtccaggca	gctggagagg	taggggtact	gaccggccac	60
717	tcccagaaat	cacgtaggct	acccctggaa	gagaagcagt	tggaggagga	ggattcctct	120
719	gccacttccg	aagaaggagg	aggagggcct	ggcccagaag	cttactcaa	caagggcctg	180
721	gccaagcacc	tgtctgagtg	tttgggggac	cgactctgcc	gcctgctgcg	gaaggagcgg	240
723	gaggcccttg	cctgggcaca	gcgagaaggc	cagggggccag	ccatgacaga	ggacagccca	300
725	ggcattccac	attgctgcag	ccgatgccac	cacggactct	tcaacaccca	ctggagatgt	360
727	tcccactgta	gccaccggct	gtgtgtagcc	tgtggtcgca	tagccggcgc	tggaaagaac	420
729	agggagaaaa	caggttctca	ggaacagcac	acagatgact	gcgcccagga	ggctgggcat	480
731	actgcctggt	ccctgatact	gaccagttt	gtctccagcc	aggcgctggc	agaactgagc	540
733	actgtgatgc	accaagcctg	ggccaagttt	gacattcggt	ggcactgttt	ctgccaggtt	600
735	gatgcccgtg	tgtgggcccc	cggggatggg	ggtcagcaga	aggaaccaac	agagaaaact	660
737	cccccaactc	cacaaccttc	ctgcaatgga	gattccaatc	ggaccaagga	catcaaagaa	720
739	gagaccccag	actccactga	gagcccagca	gaggacgggt	ctggccgggtc	accccttctc	780
741	tgtccctctc	tctgtgagct	gctagcctct	actgctgtca	aactctgcct	ggggcatgac	840
743	cggattcaca	tggcctttgc	tccggtcacc	ccagctctgc	ccagtgatga	ccgcattacc	900
745	aacatcctgg	acagcattat	tgcgcaggta	gtagaacgga	agatccaaga	gaaagccctg	960
747	gggccaggcc	tgcgagcagg	gtcaggctta	cgcaagggcc	tgagccttcc	attgtcacca	1020
749	gtgcgaaccc	ggctgtctcc	tcctggagct	ttgctgtggc	tgcaggagcc	taggcctaag	1080
751	catggcttcc	atctcttcca	ggaacactgg	cggcagggcc	agcccgtggt	agtgtcaggc	1140
753	atccagaaga	cattgagact	tagcctgtgg	ggaatggaag	cccttgggac	acttgggtggc	1200
755	caggtgcagt	cactgactgc	ccttgggcct	ccccagccca	cgaacctgga	cagcacagca	1260
757	ttctgggagg	gattctctca	tcctgagaca	cgtccaaagt	tagatgaggg	ctctgtcctc	1320
759	ctgctacacc	gaacctggg	ggataaggac	gctagcaggg	tgcagaacct	tgtctccagc	1380
761	cttccactcc	cagaatactg	tgccaccaca	gggaaactca	acctagcgtc	ctacctcccc	1440
763	ctgggcctca	cactgcatcc	actggagccc	cagctctggg	cggcctatgg	tgtgaactca	1500
765	caccgtggac	acctggggac	caagaatcta	tgcgtggagg	tgtctgacct	aatcagtatc	1560
767	ctggtgcacg	ccgaggccca	gctgcctccc	tggtatcgag	cacagaaaga	tttctctcca	1620
769	ggcctggatg	gggaaggact	ctggtctcca	gggagccaga	ccagcactgt	gtggcatgtg	1680
771	ttccggggcc	aggatgcccc	gcgcatacgt	cgttttctcc	agatggtgtg	cccagctgga	1740

invalid
 <2137
 response

RAW SEQUENCE LISTING

DATE: 05/02/2006

PATENT APPLICATION: US/10/712,629C

TIME: 14:30:25

Input Set : A:\PTO.TS.txt

Output Set: N:\CRF4\05022006\J712629C.raw

```
773 gcaggaacct tggagcctgg tgccccaggc agctgctact tggatgcagg gttgcgccga 1800
775 cggctaagag aagagtgggg tgtgagctgc tggaccctgc tgcaggctcc tggggaagcg 1860
777 gtgctggtcc cggctggggc gccccatcag gtgcagggcc tggtgagcac aatcagtgtc 1920
779 actcagcact ttctgtctcc tgagacctct gccctctctg ctcagctctg ccaccagggg 1980
781 gccagcctac cccctgacca ccgtatgctt tatgcccaga tggaccgggc tgtgttccaa 2040
E--> 783 gcagtaaagg cggctgtggg ggcgttacag gaagctaaa 2079 ←
```

see P. 5 for more error

10/7/2,629c 5

<210> 19

<211> 30

<212> DNA

<213> Oligonucleotide primer

invalid <213> response

<400> 19

ccggaattcg tcacccagtg ccaaagctgt

30

<210> 20

<211> 49

<212> DNA

<213> Oligonucleotide primer

same error

VERIFICATION SUMMARY

DATE: 05/02/2006

PATENT APPLICATION: US/10/712,629C

TIME: 14:30:26

Input Set : A:\PTO.TS.txt

Output Set: N:\CRF4\05022006\J712629C.raw

L:527 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:704 M:301 E: (44) No Sequence Data was Shown, SEQ ID:17
L:704 M:252 E: No. of Seq. differs, <211> LENGTH:Input:2079 Found:0 SEQ:17
L:711 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:783 M:301 E: (44) No Sequence Data was Shown, SEQ ID:18
L:783 M:252 E: No. of Seq. differs, <211> LENGTH:Input:693 Found:0 SEQ:18